

1/23

SEQUENCE LISTING

<110> Virax Development Pty Ltd

<120> A viral vector and methods of using same

<130> 12521330/JEH

<150> AU 2003905642

<151> 2003-10-15

<150> AU 2003905683

<151> 2003-10-16

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 1329

<212> DNA

<213> Human immunodeficiency virus

<220>

<221> CDS

<222> (1)..(1329)

<223>

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys	
20 25 30	
cat ata gta tgg gca agc agg gag cta gaa cga ttc gca gtc aat cct	144
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro	
35 40 45	
ggc ctg tta gaa aca tca gaa ggc tgc aga caa ata ttg gga cag cta	192
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu	
50 55 60	
cag cca tcc ctt cag aca gga tca gaa gaa ctt aga tca tta tat aat	240
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn	
65 70 75 80	
aca gta gca acc ctc tat tgt gta cat caa agg ata gat gta aaa gac	288
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp	
85 90 95	
acc aag gaa gct tta gag aag ata gag gaa gag caa aac aaa agt aag	336
Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys	
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cag gtc agc caa aat tac cct ata gtg cag aac cta cag ggg caa atg Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met 130 135 140	432
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tta tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr 180 185 190	576
gtg ggg gga cat caa gca gcc atg caa atg tta aaa gag act atc aat Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn 195 200 205	624
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act act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro 245 250 255	768
cct atc cca gta gga gaa atc tat aaa aga tgg ata atc ctg gga tta Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu 260 265 270	816
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 Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala
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 Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp
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 His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45
 Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60
 Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp
 85 90 95

Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
 100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Ala Ala Gly Thr Gly Asn Ser Ser
 115 120 125

Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met
 130 135 140

Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
 145 150 155 160

Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
 165 170 175

Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
 180 185 190

Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn
 195 200 205

Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro
 210 215 220

Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly
 225 230 235 240

Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro
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Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu
 260 265 270

Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg
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Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
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Thr Leu Arg Ala Glu Gln Ala Ser Gln Asp Val Lys Asn Trp Met Thr

305 310 315 320
 Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu
 325 330 335
 Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys
 340 345 350
 Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala
 355 360 365
 Met Ser Gln Val Thr Asn Pro Ala Asn Ile Met Met Gln Arg Gly Asn
 370 375 380
 Phe Arg Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu
 385 390 395 400
 Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp
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 tct tca gag cag acc aga gcc aac agc ccc acc aga aga gag ctt cag 96
 Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln
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 Val Trp Gly Gly Glu Asn Asn Ser Leu Ser Glu Ala Gly Ala Asp Arg

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Pro Leu Val Thr Ile Arg Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu															
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85 90 95															
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Lys Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val															
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Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu															
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210 215 220															
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Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln															
225 230 235 240															
gac ttc tgg gaa gtt cag tta gga ata cca cac ccc gca ggg tta aaa	768														
Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys															
245 250 255															
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260 265 270															

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aaa atc tta gag cct ttt aga aaa cag aat cca gac ata gtt atc tat Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr 325 330 335	1008
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cca cta aca gaa gaa gca gag cta gaa ctg gca gaa aac agg gag att Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile 450 455 460	1392
cta aaa gaa cca gta cat gaa gta tat tat gac cca tca aaa gac tta Leu Lys Glu Pro Val His Glu Val Tyr Tyr Asp Pro Ser Lys Asp Leu 465 470 475 480	1440
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gcc agc tgt gat aaa tgt cag cta aaa gga gaa gcc atg cat gga caa	2304
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755 760 765	
gta gac tgt agt cca gga ata tgg caa cta gat tgt aca cat cta gaa	2352
Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr His Leu Glu	
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Gly Lys Ile Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu	
785 790 795 800	
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Ala Glu Val Ile Pro Ala Glu Thr Gly Gln Glu Thr Ala Tyr Phe Leu	
805 810 815	
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Leu Lys Leu Ala Gly Arg Trp Pro Val Lys Thr Ile His Thr Asp Asn	
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Gly Ser Asn Phe Thr Ser Thr Thr Val Lys Ala Ala Cys Trp Trp Ala	
835 840 845	
ggg atc aag cag gaa ttt ggc att ccc tac aat ccc caa agt caa gga	2592
Gly Ile Lys Gln Glu Phe Gly Ile Pro Tyr Asn Pro Gln Ser Gln Gly	
850 855 860	
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Val Val Glu Ser Met Asn Asn Glu Leu Lys Lys Ile Ile Gly Gln Val	
865 870 875 880	
aga gat cag gct gaa cac ctt aag aca gca gta caa atg gca gta ttc	2688
Arg Asp Gln Ala Glu His Leu Lys Thr Ala Val Gln Met Ala Val Phe	
885 890 895	
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Ile His Asn Phe Lys Arg Lys Gly Gly Ile Gly Gly Tyr Ser Ala Gly	
900 905 910	
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Glu Arg Ile Val Asp Ile Ile Ala Thr Asp Ile Gln Thr Lys Glu Leu	
915 920 925	
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Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Asp	
930 935 940	
aac aaa gat ccc ctt tgg aaa gga cca gca aag ctt ctc tgg aaa ggt	2880
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10/23

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aga aga aaa gca aaa atc att agg gat tat gga aaa cag atg gca ggt							2976
Arg Arg Lys Ala Lys Ile Ile Arg Asp Tyr Gly Lys Gln Met Ala Gly							
		980		985		990	
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<210> 4
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 <212> PRT
 <213> Human immunodeficiency virus

<400> 4

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Val Trp Gly Gly Glu Asn Asn	Ser Leu Ser Glu Ala Gly Ala Asp Arg
35	40 45
Gln Gly Thr Val Ser Phe Asn	Phe Pro Gln Ile Thr Leu Trp Gln Arg
50	55 60
Pro Leu Val Thr Ile Arg Ile	Gly Gly Gln Leu Lys Glu Ala Leu Leu
65	70 75 80
Asp Thr Gly Ala Asp Asp Thr	Val Leu Glu Glu Met Asn Leu Pro Gly
85	90 95
Lys Trp Lys Pro Lys Met Ile	Gly Gly Ile Gly Gly Phe Ile Lys Val
100	105 110
Arg Gln Tyr Asp Gln Ile Pro	Val Glu Ile Cys Gly His Lys Ala Ile
115	120 125
Gly Thr Val Leu Val Gly Pro	Thr Pro Val Asn Ile Ile Gly Arg Asn
130	135 140

Leu Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe Pro Ile Ser Pro Ile
 145 150 155 160

Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val
 165 170 175

Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile
 180 185 190

Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu
 195 200 205

Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr
 210 215 220

Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln
 225 230 235 240

Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys
 245 250 255

Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser
 260 265 270

Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro
 275 280 285

Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu
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Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr
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 325 330 335

Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln
 340 345 350

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
 355 360 365

12/23

Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
370 375 380

Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Met
385 390 395 400

Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val
405 410 415

Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys Val Lys
420 425 430

Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile
435 440 445

Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile
450 455 460

Leu Lys Glu Pro Val His Glu Val Tyr Tyr Asp Pro Ser Lys Asp Leu
465 470 475 480

Val Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln Ile
485 490 495

Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala Arg Met
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Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln
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530 535 540

Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Ala Trp Trp Met Glu Tyr
545 550 555 560

Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro
565 570 575

Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val Gly Ala
580 585 590

Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly
 595 600 605
 Lys Ala Gly Tyr Val Thr Asp Arg Gly Arg Gln Lys Val Val Ser Ile
 610 615 620
 Ala Asp Thr Thr Asn Gln Lys Thr Glu Leu Gln Ala Ile His Leu Ala
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 645 650 655
 Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp Lys Ser Glu Ser Glu Leu
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 Val Ser Gln Ile Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu
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 Lys Leu Val Ser Ala Gly Ile Arg Lys Val Leu Phe Leu Asn Gly Ile
 705 710 715 720
 Asp Lys Ala Gln Glu Glu His Glu Lys Tyr His Ser Asn Trp Arg Ala
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 Met Ala Ser Asp Phe Asn Leu Pro Pro Val Val Ala Lys Glu Ile Val
 740 745 750
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